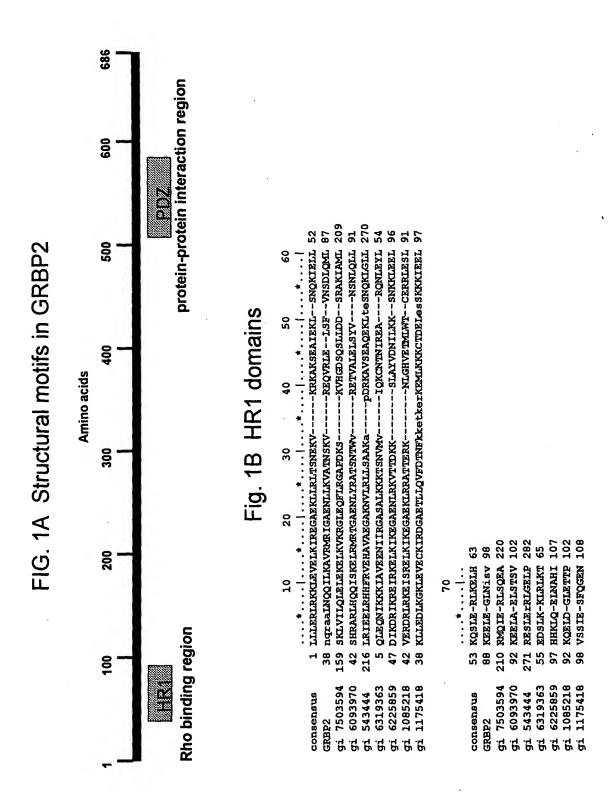
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Fig. 1C PDZ domains

		30 40
consensus	н	* * * * * Eprivelekggggigfsinggkdsggggvvvssvvpgspakag- 44
GRBP2	513	pprsiretaregdlgetirgnapvqvhfidpycsasvag- 551
gi 13096475	70	PSRLAALRRGTagsvTGVGLEITYDGGSGKOVVVLTPAPGGPAEKAG- 116
gi 7512038	405	epreisfokegsvgirliggneagievtavopgsdaslog- 444
gi 6671754	484	EPRIVEIIREL8DALGISIAGGKGSP1gdipifiamioangvaartok 531
gi. 7662086	44	VQRCVIIQKDQHGFGFTVSGDRIVLVQSVRPGGAANKAG- 82
gi 131530	507	YLVLIRITEDedGKEGENIKGGVDQkMPLVVSRINPESPADTCIP 551
gi 6093970	497	LVGPVHMTRGEGGFGFTLRGDSPVLIAAVVPGGQAESAG- 535
gi 7499828	46	RPHVVKVVKSETGFGFNVKGQVSEGgqlrslngqlyaPlQHVSAVLRRGAADQAG- 100
gi 8247939	410	IHVTILHKEEGAGLGFSLAGGADIEnKVITVHRVFPNGLASQEGt 454
		70 80 90 100

consensus	45	
GRBP2	552	-AREGDYIVSIQL-VDCKWLTLSEVMKCLKSfGEDEIEMKVVs11 594
gi 13096475	117	-ARACDVIVIVOG-TAVKGLSLYDVSDLLQG-EADsQVEVVLHAPG 159
gi 7512038	445	-IMPGDKILKVND-MOMNGVTREEAVIFILS-LQDRIDLIVQYCK 486
gi 6671754	532	-LKVGDRIVSING-QPIDGLSHTDAVNILKN-AFGRIILQVVADT 573
gi 7662086	83	-VKEGDRIIKVNGtMVTNSS-HLEVVKLIKSGarvaltilgss 123
gi 131530	552	kinegdoivlingr-disehthdovvmfika-sreshsfelalvirrra 598
gi 6093970	536	-ikecdyivsvng-opckmmkhlevvtolks-mgeegvslovysll 578
gi 7499828	101	
gi 8247939	455	-iqkgnevising-ksikgtthhdalaiirq-areprqavivtrki 497

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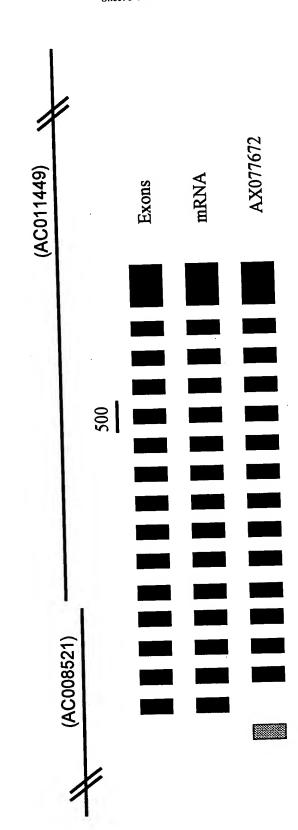


FIG. 2
Genomic structure of human GRBP2

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Fig. 3

Nucleotide and protein sequence of the GRBP2 gene

nt: SEQ ID NO: 1
aa: SEQ ID NO: 3

tc	cgc	gcc	cgc	gcc	gct	agc			L CTG	L TTG	6 38
		A GCC		-							19 77
Y TAC		R CGG								G GGC	32 116
R CGG		K AAA		_		_				Q CAG	45 155
		L CTG								E GAA	58 194
		L CTG									71 233
		R CGG									84 272
_		L CTC								S TCG	97 311
		V GTC		_							110 350
		I ATT									124 389
		A GCA									137 428
Y TAC	_	E GAA								A GCA	150 467
D GAT	L CTT					_			P CCT	S AGC	163 506

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												F TTC	
											P CCG		189 584
											D GAC		201 623
											L CTG		214 662
											L CTC		227 701
	_										Q CAG		240 740
G GGG								F TTT				A GCA	253 779
											H CAT		266 818
											V GTG		279 857
								_			V GTG		292 896
											F TTC		305 935
						-		A GCT				G GGA	
E GAG	V GTC	Y TAC	Q CAA	Q CAG	L CTA	H CAC	A GCA	A GCC	M ATG	S AGC	Q CAG	A GCG	331 1013
P CCG	V GTG	K AAA	E GAG	N AAC	I ATC	P CCC	Y TAC	S TCC	W TGG	A GCC	S AGC	L TTA	344 1052
													357 1091
Y TAC	F TTC	T ACT	A GCC	I ATC	L CTC	L CTC	I ATC	D GAC	H CAC	Q CAG	V GTG	K AAG	370 1130

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P CCA	G GGC	T ACG	D GAT	L CTG	D GAC	H CAC	Q CAG	E GAG	K AAG	C TGC	L CTG	S TCC	383 1169
											P CCC	L TTG	396 1208
											L CTG		409 1247
											E GAG	E GAG	422 1286
											R CGG	S AGC	.435 1325
I ATT				_								E GAA	
R CGC												D GAT	
												A GCT	
												F TTC	487 1481
												G GGC	500 1520
			V GTG									P CCT	
P CCT												L TTG	
G GGG	F TTC	T ACC	L TTG	R AGA	G GGG	N AAC	A GCC	P CCC	V	Q CAG	V GTT	H CAC	539 1637
F TTC	L CTG	D GAT	P CCT	Y TAC	C TGC	S TCT	A GCC	S TCG	V GTG	A GCA	G GGA	A GCC	552 1676
R CGG	E GAA	G GGA	D GAT	Y TAT	I ATT	V GTC	S TCC	I ATT	Q CAG	L CTT	V GTG	D GAT	565 1715
													578 1754

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												V GTG	591 1793
												S AGT	
							Q CAG					M ATG	617 1871
							D GAC					K AAA	630 1910
T ACC		K AAA					L CTT					W TGG	643 1949
G GGC	T ACC						K AAG					L TTG	
												K AAG	
												D gac	
			Y tac		tgt	gag	gaa	aca	aac	atg	ttc	agg	686 2105
ccc	cga	aca	ttt	ccg	gtg	ctg	act	cgg	cct	taa	acg	ttt.	2144
gtg	cca	taa	tgg	aaa	ata	tct	atc	tat	ctg	ttg	tca	aat	2183
cct	gtt	ttt	ctc	ata	gtg	taa	act	cac	att	tga	tgt	gtt	2222
ttt	atg	aag	gaa	agt	aac	caa	gaa	acc	tct	agg	aat	tag	2261
tga	aaa	aag	aac	ttt	ttt	gag	gtg	tgt	tac	tat	act	gct	2300
gta	agt	tat	tta	tta	tat	aaa	gta	ttg	taa	ata	gaa	tag	2339
tgt	tga	aga	tat	gaa	ata	tgg	cta	ctt	tta	atg	gtg	aca	2378
att	atg	act	ttt	agt	cac	tat	taa	att	ggg	gtt	acc	tat	2417
atc	agt	aca	att	tgt	agt	tgt	ttc	cag	gtt	tgg	cta	ata	2456
atc	att	cct	taa	cct	aga	att	cag	atg	atc	ctg	gaa	tta	2495
agg	cag	gtc	aga	gga	ctg	taa	tga	tag	aat	taa	att	agt	2534
gtc	act	aaa	aac	tgt	ccc	aaa	gtg	ctg	ctt	cct	aat	agg	2573

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aat	tca	tta	acc	taa	aac	aag	atg	tta	cta	tta	tat	cga	2612
tag	acț	atg	aat	gct	att	tct	aga	aaa	agt	cta	gtg	cca	2651
aat	ttg	tct	tat	taa	ata	aaa	aca	atg	tag	gag	cag	ctt	2690
ttc	ttc	tag	ttt	gat	gtc	att	taa	gaa	tta	cta	aca	cag	2729
tgg	cag	tgt	tag	atg	aag	atg	ctg	tct	aca	agg	tag	ata	2768
ata	tac	tgt	ttg	ata	ctc	aaa	aca	ttt	ttc	att	ttg	ttt	2807
aaa	gta	gaa	gtt	aca	taa	ttc	tat	att	tta	agt	ctt	ggg	2846
taa	aaa	agt	agt	ttt	aca	ttt	tat	aaa	gta	aag	atg	taa	2885
atg	att	cag	gtt	taa	agc	tct	att	tga	ctt	cct	ttt	ttt	2,924
gtt	tga	gat	agc	gtc	ttg	ctg	tgt	tgc	сса	ggc	tgg	agt	2963
gca	gtg	gtg	tga	tct	cag	ctc	agt	gca	acc	tcc	gcc	ccc	3002
tgg	gat	caa	gcg	att	ctc	cta	cct	cag	cct	ccc	aaa	tag	3041
ctg	gga	cta	caa	ggt	gcc	ctc	cag	cat	gcc	tgg	ctg	att	3080
ttt	gta	ttt	tta	gtt	gag	gtg	agg	ttt	cac	cat	gtt	ggc	3119
cag	gcg	ggt	ttc	gaa	atc	ctg	acc	tca	aat	gat	cca	ccc	3158
acc	tca	gcc	tcc	caa	agt	gct	ggg	att	aca	ggc	atg	agc	3197
cac	cac	aac	cgt	ccc	act	att	tta	ctt	ttt	aaa	atg	aca	3236
ttc	cta	ctg	att	gat	ttt	tat	ctt	gct	ata	agt	tcg	atg	3275
aca	ccg	tga	atc	taa	taa	ggt	tca	ctg	ttg	aca	cag	tac	3314
aag	tta	cat	agc	taa	aat	aca	tag	cat	tga	aga	cta	att	3353
tta	agg	att	gac	aag	agt	tta	ttt	tct	att	gtg	caa	tat	3392
ctt	aaa	gga	agc	aac	cac	ctt	tgg	gaa	agt	gta	tct	gct	3431
gct	cct	agg	gcc	atg	ctt	gta	tac	ata	ttt	aaa	taa	aca	3470
tat	tca	ttt	acc	cg									3484